

P. HAMBEL

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1644

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/339,922A

DATE: 11/20/2000
TIME: 10:41:25

Input Set : A:\IX3536.txt
Output Set: N:\CRF3\11202000\I339922A.raw

P.5

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3 <110> APPLICANT: Huse, William D.
4   Wu, Herren
6 <120> TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
7   Acids Encoding Same and Methods of Use
9 <130> FILE REFERENCE: P-IX 3536
11 <140> CURRENT APPLICATION NUMBER: US 09/339,922A
12 <141> CURRENT FILING DATE: 1999-06-24
14 <160> NUMBER OF SEQ ID NOS: 112
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 351
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
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24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(351)
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
29   antibody variable region
31 <400> SEQUENCE: 1
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33   Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
34   1           5           10           15
36   tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat   96
37   Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
38   1           20           25           30
40   gac atg tct tgg gtt cgc cag gct ccg ggc aag ggt ctg gag tgg gtc   144
41   Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
42   35           40           45
44   gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtc   192
45   Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
46   50           55           60
48   cag ggc cga ttc acc atc tcc aga gac aat agt aag aac acc cta tac   240
49   Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
50   65           70           75           80
52   ctg caa atg aac tct ctg aga gcc gag gac aca gcc gtg tat tac tgt   288
53   Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
54   85           90           95
56   gca aga cat aac tac ggc agt ttt gct tac tgg ggc caa ggg act aca   336
57   Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
58   100          105          110
60   gtg act gtt tct agt   351
61   Val Thr Val Ser Ser
62   115
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 117
67 <212> TYPE: PRT
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68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
72     antibody variable region
74 <400> SEQUENCE: 2
75 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
76   1           5           10           15
78 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
79           20           25           30
81 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
82   35           40           45
84 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
85   50           55           60
87 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
88   65           70           75           80
90 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
91           85           90           95
93 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
94   100          105          110
96 Val Thr Val Ser Ser
97   115
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 321
103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (1)..(321)
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
112     antibody variable region
114 <400> SEQUENCE: 3
115 gag att gtg cta act cag tct cca gcc acc ctg tct ctc agc cca gga   48
116 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
117   1           5           10           15
119 gaa agg gcg act ctt tcc tgc cag gcc agc caa agt att agc aac cac   96
120 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
121           20           25           30
123 cta cac tgg tat caa caa agg cct ggt caa gcc cca agg ctt ctc atc   144
124 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
125           35           40           45
127 aag tat cgt tcc cag tcc atc tct ggg atc ccc gcc agg ttc agt ggc   192
128 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
129           50           55           60
131 agt gga tca ggg aca gat ttc acc ctc act atc tcc agt ctg gag cct   240
132 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
133   65           70           75           80
135 gaa gat ttt gca gtc tat tac tgt caa cag agt ggc agc tgg cct cac   288
136 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His

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137                               85                               90                               95
139 acg ttc gga ggg ggg acc aag gtg gaa att aag                               321
140 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
141                               100                               105
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 107
146 <212> TYPE: PRT
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
151     antibody variable region
153 <400> SEQUENCE: 4
154 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
155 1                               5                               10                               15
157 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
158                               20                               25                               30
160 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
161                               35                               40                               45
163 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
164                               50                               55                               60
166 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
167 65                               70                               75                               80
169 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
170                               85                               90                               95
172 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
173                               100                               105
177 <210> SEQ ID NO: 5
178 <211> LENGTH: 351
179 <212> TYPE: DNA
180 <213> ORGANISM: Mus musculus
182 <220> FEATURE:
183 <221> NAME/KEY: CDS
184 <222> LOCATION: (1)..(351)
186 <400> SEQUENCE: 5
187 gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga agg 48
188 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
189 1                               5                               10                               15
191 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc gct ttc agt agc tat 96
192 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
193                               20                               25                               30
195 gac atg tct tgg gtt cgc cag att ccg gag aag agg ctg gag tgg gtc 144
196 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
197                               35                               40                               45
199 gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg 192
200 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
201                               50                               55                               60
203 cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc cta tac 240
204 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
205 65                               70                               75                               80

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Output Set: N:\CRF3\11202000\I339922A.raw

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207 ctg caa atg agc agt ctg aac tct gag gac aca gcc atg tat tac tgt 288
208 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
209                               85                               90                               95
211 gca aga cat aac tac ggc agt ttt gct tac tgg qgc caa ggg act ctg 336
212 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
213                               100                               105                               110
215 gtc act gtc tct gca 351
216 Val Thr Val Ser Ala
217 115
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 117
222 <212> TYPE: PRT
223 <213> ORGANISM: Mus musculus
225 <400> SEQUENCE: 6
226 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
227 1 5 10 15
229 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
230 20 25 30
232 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
233 35 40 45
235 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
236 50 55 60
238 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
239 65 70 75 80
241 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
242 85 90 95
244 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
245 100 105 110
247 Val Thr Val Ser Ala
248 115
252 <210> SEQ ID NO: 7
253 <211> LENGTH: 321
254 <212> TYPE: DNA
255 <213> ORGANISM: Mus musculus
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (1)..(321)
261 <400> SEQUENCE: 7
262 gat att gtg cta act cag tct cca gcc acc ctg tct gtg aca cca gga 48
263 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
264 1 5 10 15
266 gat agc gtc agt ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
267 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
268 20 25 30
270 cta cac tgg tat caa caa aaa tca cat gag tct cca agg ctt ctc atc 144
271 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
272 35 40 45
274 aag tat cgt tcc cag tcc atc tct ggg atc ccc tcc agg ttc agt ggc 192
275 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly

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276      50      55      60
278 agt gga tca ggg aca gat ttc gct ctc agt atc aac agt gtg gag act 240
279 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
280 65      70      75      80
282 gaa gat ttt gga atg tat ttc tgt caa cag agt ggc agc tgg cct cac 288
283 Glu Asp Phe Gly Met Tyr Phe Cys Gln Glu Ser Gly Ser Trp Pro His
284      85      90      95
286 acg ttc gga ggg acc aag ctg gaa att aag 321
287 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
288      100      105
291 <210> SEQ ID NO: 8
292 <211> LENGTH: 107
293 <212> TYPE: PRT
294 <213> ORGANISM: Mus musculus
296 <400> SEQUENCE: 8
297 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
298 1      5      10      15
300 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
301      20      25      30
303 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
304      35      40      45
306 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
307      50      55      60
309 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
310 65      70      75      80
312 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
313      85      90      95
315 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
316      100      105
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 84
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence:
327     oligonucleotide
329 <400> SEQUENCE: 9
330 caggtgcagc tgggtgagtc tgggggaggc gttgtgcagc ctggaaggct cctgagactc 60
331 tccgtgtcag cctctggatt cacc 84
334 <210> SEQ ID NO: 10
335 <211> LENGTH: 84
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Description of Artificial Sequence:
341     oligonucleotide
343 <400> SEQUENCE: 10
344 aacttttgcg acccaactcca gacccttgcc cggagcctgg cgaacccaag acatgtcata 60
345 gctactgaag gtgaatccag aggc 84

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/339,922A

DATE: 11/20/2000

TIME: 10:41:26

Input Set : A:\IX3536.txt

Output Set: N:\CRF3\11202000\I339922A.raw

L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32